● ● **1647**

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,177C*

DATE: 04/01/2001
TIME: 07:37:03

INPUT SET: S36583.raw

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

pp 2,4

Does Not Comply
Corrected Diskette Needed

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```
 1                                       SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5      (i) APPLICANT:  Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
 6
 7     (ii) TITLE OF INVENTION:   ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
 8          IT, AND USES THEREOF
 9
10    (iii) NUMBER OF SEQUENCES: 46
11
12     (iv) CORRESPONDENCE ADDRESS:
13          (A) ADDRESSEE:  Fulbright & Jaworski L.L.P.
14          (B) STREET:     666 Fifth Avenue
15          (C) CITY:       New York City
16          (D) STATE:      New York
17          (E) COUNTRY:    USA
18          (F) ZIP:        10103
19
20      (v) COMPUTER READABLE FORM:
21          (A) MEDIUM TYPE:  Diskette, 3.25 inch, 1.44mb
22          (B) COMPUTER:  IBM PS/2
23          (C) OPERATING SYSTEM:  PC-DOS
24          (D) SOFTWARE:  Wordperfect
25
26     (vi) CURRENT APPLICATION DATA:
27          (A) APPLICATION NUMBER: 09/039,177
28          (B) FILING DATE: March 13, 1998
29          (C) CLASSIFICATION: 435
30
31    (vii) PRIOR APPLICATION DATA:
32          (A) APPLICATION NUMBER:  PCT/GB93/02367
33          (B) FILING DATE: November 17, 1993
34
35    (vii) PRIOR APPLICATION DATA:
36          (A) APPLICATION NUMBER: GB 9224057.1
37          (B) FILING DATE: November 17, 1992
38
39    (vii) PRIOR APPLICATION DATA:
40          (A) APPLICATION NUMBER: GB 9304677.9
41          (B) FILING DATE: March 8, 1993
42
43    (vii) PRIOR APPLICATION DATA:
44          (A) APPLICATION NUMBER: GB 9304680.3
45          (B) FILING DATE: March 8, 1993
```

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INPUT SET: S36583.raw

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 46
 47     (vii)  PRIOR APPLICATION DATA:
 48              (A) APPLICATION NUMBER: 9311047.6
 49              (B) FILING DATE: May 28, 1993
 50
 51     (vii)  PRIOR APPLICATION DATA:
 52              (A) APPLICATION NUMBER: 9313763.6
 53              (B) FILING DATE: July 2, 1993
 54
 55     (vii)  PRIOR APPLICATION DATA:
 56              (A) APPLICATION NUMBER: 9136099.2
 57              (B) FILING DATE: August 3, 1993
 58
 59     (vii)  PRIOR APPLICATION DATA:
 60              (A) APPLICATION NUMBER: 321344.5
 61              (B) FILING DATE: October 15, 1993
 62
 63     (viii) ATTORNEY/AGENT INFORMATION:
 64              (A) NAME: Mary Anne Schofield
 65              (B) REGISTRATION NUMBER: 36,669
 66              (C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS
 67
 68      (ix)  TELECOMMUNICATION INFORMATION:
 69              (A) TELEPHONE: (202) 662-0200
 70              (B) TELEFAX:   (202) 662-4643
 71
 72
 73
```

ERRORED SEQUENCES FOLLOW:

```
2717    (2) INFORMATION FOR SEQ ID NO: 34:
2718         (i) SEQUENCE CHARACTERISTICS:
2719              (A) LENGTH: 513 amino acids
2720              (B) TYYPE: amino acid
2721              (D) TOPOLOGY: linear
2722
2723        (ii) MOLECULE TYPE: peptide
2724
2725        (vi) ORIGINAL SOURCE:
2726              (A) ORGANISM: MOUSE
2727
2728        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
2729
2730
2731    Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
2732                     5                  10                  15
2733    Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
2734                    20                  25                  30
2735    Phe Asn Ala Asn Trp Glu lys Asp Arg Thr Asn Gln Thr Gly Val Glu
```

--> 2720

) format err: delete "7"

```
2736            35                     40                     45
2737    Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
2738            50          \          55                     60
2739    Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
2740    65                      70                     75                  80
2741    Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
2742                    85                     90                     95
2743    Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
2744                    100                    105                    110
2745    Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
2746            115                    120                    125
2747    Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
2748            130                    135                    140
2749    Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
2750    145                    150                    155                    160
2751    Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
2752                    165                    170                    175
2753    Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
2754            180                    185                    190
2755    Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
2756            195                    200                    205
2757    Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
2758            210                    215                    220
2759    Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
2760    225                    230                    235                    240
2761    Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
2762                    245                    250                    255
2763    Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
2764                    260                    265                    270
2765    Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
2766            275                    280                    285
2767    Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
2768            290                    295                    300
2769    Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
2770    305                    310                    315                    320
2771    Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
2772                    325                    330                    335
2773    Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
2774                    340                    345                    350
2775    Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
2776            355                    360                    365
2777    Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
2778            370                    375                    380
2779    Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
2780    385                    390                    395                    400
2781    Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
2782                    405                    410                    415
2783    Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
2784                    420                    425                    430
2785    Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
2786            435                    440                    445
2787    Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
2788            450                    455                    460
```

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```
2789   Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
2790   465             470             475             480
2791   Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
2792                   485             490             495
2793   Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
2794               500             505             510
2795   Leu
2796
2797
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```
2970   (2)  INFORMATION FOR SEQ ID NO: 37:
2971        (i)  SEQUENCE CHARACTERISTICS:          → 97 shown
2972             (A)  LENGTH: (102) amino acids
2973             (B)  TYPE? amino acid              → delete "7"
2974             (D)  TOPOLOGY: linear
2975
2976        (ii) MOLECULE TYPE: peptide
2977
2978        (vi) ORIGINAL SOURCE:
2979             (A)  ORGANISM: C. elegans
2980
2981        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
2982
2983
2984   Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp
2985                                               5                   10
2986   Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu
2987                                   20              25              30
2988   Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser
2989                                               35              40
2990   Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp
2991                                       50          55          60
2992   Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr
2993                                               65              70
2994   Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe
2995                                                   85          90
2996   Cys
2997
2998
2999
```

misaligned amino acid nos.
(see item 4 on Error Summary sheet)

```
3125   (2)  INFORMATION FOR SEQ ID NO:46:
3126        (i)  SEQUENCE CHARACTERISTICS:
3127             (A)  LENGTH:? amino acids       mandatory response needed (6 shown)
3128             (B)  TYPE: amino acid
3129             (D)  TOPOLOGY: linear
3130
3131        (ii) MOLECULE TYPE: peptide
3132
3133        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3134
3135   Gly Thr Ala Arg Tyr Met
3136                        ≠5
```

misaligned number

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/039,177C*

INPUT SET: S36583.raw

Line	Error	Original Text
29	Wrong Classification	(C) CLASSIFICATION: 435
2720	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
2972	Entered (102) and Calc. Seq. Length (97) differ	(A) LENGTH: 102 amino acids
2973	Unknown or Misplaced Identifier	(B) TY7PE: amino acid
3127	Length must be an Integer	(A) LENGTH: amino acids
3127	Entered (0) and Calc. Seq. Length (6) differ	(A) LENGTH: amino acids

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Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION

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ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _✓_ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.